Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently amended) A method for displaying genotype information associated with probe array experiments, comprising the acts of:

receiving one or more sets of emission intensity data, wherein each set of emission intensity data includes a plurality of emission intensity values from a probe array experiment with an individual sample and each emission intensity value is associated with a probe disposed upon a probe array;

generating a plurality of genotype calls for each set of emission intensity data, wherein each of the genotype calls is generated by applying one or more of the emission intensity values to one or more models enabled to specify nucleic acid composition, the models include a no call model, a homozygote model, and a heterozygote model;

assembling the plurality of genotype calls for each set of emission intensity data into one or more genotype data sets; ~~and~~

displaying ~~one or more~~ a plurality of the genotype calls of each of the genotype data sets to a user in a graphical user interface comprising a first pane that displays a graphical representation of a first region of sequence associated with the genotype data sets, a second pane that displays a graphical representation of a second region of sequence selected from the first region of sequence, and a third pane that displays a graphical representation of a third region of sequence selected from the second region of sequence, wherein the graphical representation of the second region includes greater

detail than the graphical representation of the first region, the graphical representation of the third region includes greater detail then the graphical representation of the second region and comprises a representation of sequence composition including the one or more genotype calls of each genotype data set~~.~~ ; and

color coding the displayed sequences from a plurality of different samples in the first, second, or third panes to identify a plurality of calls, consisting of heterozygous calls, homozygous calls, and no calls.

2. (Original) The method of claim 1, wherein:

each of the plurality of emission intensity values corresponds to detected emissions from a scanned probe array.

3. (Original) The method of claim 1, wherein:

the probe includes a genotyping probe.

4. (Original) The method of claim 3, wherein:

the genotyping probe includes a sequencing probe.

5. (Original) The method of claim 3, wherein:

the genotyping probe includes a SNP probe.

6. (Previously presented) The method of claim 1, wherein:

the genotype call is an A, G, C, T, or no call.

7. (Original) The method of claim 1, wherein:

the genotype call includes a SNP call.

8-12 (Cancelled)

13. (Original) The method of claim 1, further comprising the acts of:

retrieving annotation information in response to a user selection of one or more of the displayed genotype calls; and

displaying the annotation information in one or more panes of the graphical user interface.

14. (Currently amended) A system for displaying genotype information associated with probe array experiments, comprising:

a sequence data manager that receives one or more sets of emission intensity data, wherein each set of emission intensity data includes a plurality of emission intensity values from a probe array experiment with an individual sample and each emission intensity value is associated with a probe disposed upon a probe array;

a genotype call generator that generates a plurality of genotype calls for each set of emission intensity data, wherein each of the genotype calls is generated by applying one or more of the emission intensity values to one or more models enabled to specify nucleic acid composition, the models include a no call model, a homozygote model, and a heterozygote model;

a data assembler that assembles the plurality of genotype calls for each set of emission intensity data into one or more genotype data sets; and

an output manager that displays a plurality ~~one or more~~ of the genotype calls of each of the genotype data sets to a user in a graphical user interface comprising a first pane that displays a graphical representation of a first region of sequence associated with the genotype data sets, a second pane that displays a graphical representation of a second region of sequence selected from the first region of sequence, and a third pane that displays a graphical representation of a third region of sequence selected from the second region of sequence, wherein the graphical representation of the second region includes greater detail than the graphical representation of the first region, the graphical representation of the third region includes greater detail then the graphical representation of the second region and comprises a representation of sequence composition including the one or more genotype calls of each genotype data set~~.~~ , the output manager also color codes the displayed sequences from a plurality of different samples from the first, second, or third panes to identify a plurality of calls, consisting of heterozygous calls, homozygous calls, and no calls.

15. (Original) The system of claim 14, wherein:

each of the plurality of emission intensity values corresponds to detected emissions from a scanned probe array.

16. (Original) The system of claim 14, wherein:

the probe includes a genotyping probe.

17. (Original) The system of claim 16, wherein:

the genotyping probe includes a sequencing probe.

18. (Original) The system of claim 16, wherein:

the genotyping probe includes a SNP probe.

19. (Previously presented) The system of claim 14, wherein:

the genotype call is an A, G, C, T, or no call.

20. (Original) The system of claim 14, wherein:

the genotype call includes a SNP call.

21-25 (Cancelled)

26. (Original) The system of claim 14, wherein:

the output manager is further constructed and arranged to retrieve annotation information in response to a user selection of one or more of the displayed genotype calls, and display the annotation information in one or more panes of the graphical user interface.

27. (Currently amended) A computer system for displaying genotype information associated with probe array experiments, comprising:

a user computer having system memory with executable code stored thereon, wherein the executable code performs a method, comprising;

receiving one or more sets of emission intensity data, wherein each set of emission intensity data includes a plurality of emission intensity values from a probe

array experiment with an individual sample and each emission intensity value is associated with a probe disposed upon a probe array;

a genotype call generator that generates ~~generating~~ a plurality of genotype calls for each set of emission intensity data, wherein each of the genotype calls is generated by applying one or more of the emission intensity values to one or more models enabled to specify nucleic acid composition, the models include a no call model, a homozygote model, and a heterozygote model;

a data assembler that assembles ~~assembling~~ the plurality of genotype calls for each set of emission intensity data into one or more genotype data sets; and

an output manager that displays ~~displaying~~ one or more of the genotype calls of each of the genotype data sets to a user in a graphical user interface comprising a first pane that displays a graphical representation of a first region of sequence associated with the genotype data sets, a second pane that displays a graphical representation of a second region of sequence selected from the first region of sequence, and a third pane that displays a graphical representation of a third region of sequence selected from the second region of sequence, wherein the graphical representation of the second region includes greater detail than the graphical representation of the first region, the graphical representation of the third region includes greater detail then the graphical representation of the second region and comprises a representation of sequence composition including the one or more genotype calls of each genotype data set~~.~~ , the output manager also color codes the displayed sequences from a plurality of different samples from the first, second, or third panes to identify a plurality of calls, consisting of, heterozygous calls, a homozygous calls, and no calls.

28. (Cancel)

29. (Previously presented) The method of claim 1, wherein:

the graphical representations of the second and third regions of sequence comprise an alignment of sequence information of two or more of the samples.

30. (Cancel)

31. (Previously presented) The method of claim 1, wherein:

the user selects the second region of sequence.

32. (Previously presented) The method of claim 1, wherein:

the user selects the third region of sequence.

33. (Cancel)

34. (Previously presented) The system of claim 14, wherein:

the graphical representations of the second and third regions of sequence comprise an alignment of sequence information of two or more of the samples.

35. (Cancel)

36. (Previously presented) The method of claim 1, wherein:

the user selects the second region of sequence.

37. (Previously presented) The method of claim 1, wherein:

the user selects the third region of sequence.